SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:

        (A) NAME: NESTEC S.A

        (B) STREET: AVENUE NESTLE 55,

        (C) CITY: VEVEY

        (D) STATE OR PROVINCE: VAUD

        (E) COUNTRY: SWITZERLAND

        (F) POST CODE: 1800

        (G) TELEPHONE: 021 924 26 09

        (H) FAX: 021 924 28 80

    (ii) TITLE OF THE INVENTION: COFFEE MANNANASE

    (iii) NUMBER OF SEQUENCES: 7

    (iv) COMPUTER READABLE FORM

        (A) MEDIUM TYPE: Floppy disk

        (B) COMPUTER: IBM PC compatible

        (C) OPERATING SYSTEM: PC-DOS/MS-DOS

        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1613 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: double

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
TTCATTAAAA ATGGCCTTCT CCAGGAGAAG CAATATCAGC AACTTCTCTT GCTGCTTCCT      60
TGTGATCATC GTCTTATCCC TGCATTGCGA AAATCATATA GTTTCTTCTT CTGCTTCGCG     120
CTTTATTCAA ACAAGAGGAA CCCGATTCGT GTTAGGTGGC TACCCATTTT TTTTCAATGG     180
GTTCAACTCC TACTGGATGA TGCATGTTGC AGCTGAGCCA AGTGAAAGGC ATAAAATTTC     240
CAATGTATTT CGCGACGCTG CTGCTACAGG GCTTACTGTT TGCCGGACAT GGGCATTCAG     300
CGATGGTGGC GATCGAGCTC TTCAAATGTC CCCCGGAGTC TATGATGAAC GTGTCTTTCA     360
```

```
GGCCCCTTGAT TTTGTGGTAT CGGAAGCAAG GAAGTATGGA GTTCACTTAA TCCTGAGTCT    420
GACCAACAAC TACAAGGACT TTGGAGGAAG GACGCAATAC GTGACGTGGG CTAAAAATGC    480
CGGAGTACAA GTGAATAGCG ATGATGATTT TTACACCAAG AATGCTGTCA AGGGATATTA    540
CAAGAATCAC ATTAAGAAAG TGTTGACTAG GATCAACACA ATCAGTAGAG TTGCATATAA    600
AGATGATCCA ACAGTCATGG CATGGGAGCT AATAAATGAA CCTCGTTGCC AGGTCGACTT    660
CTCCGGAAAA ACCTTAAATG CTTGGGTTCA AGAAATGGCA ACTTACGTCA AATCACTCGA    720
TAACAAACAC CTTCTAGAAA TAGGCATGGA GGGATTCTAC GGAGATTCAA TGCCAGGCAA    780
AAAGCAGTAC AATCCTGGAT ACCAAGTGGG CACAGATTTT ATCACCAATA ATCTTATCAA    840
AGAGATAGAT TTTGCAACCA TTCATGCATA TCCCGATATT TGGCTGTCTG GACAGAGCGA    900
CGGTGCACAG ATGATGTTCA TGAGAAGGTG GATGACCAGT CACTCCACAG ACTCTAAGAC    960
CATACTTAAA AAACCATTGG TTCTCGCTGA ATTTGGGAAA TCAAGTAAAG ATCCAGGATA   1020
CAGTTTATAT GCCAGGGAGT CATTCATGGC CGCAATTTAC GGTGATATCT ACAGGTTTGC   1080
TAGAAGAGGA GGCATTGCAG GTGGATTGGT TTGGCAAATC CTGGCCGAGG GAATGCAACC   1140
GTACGCAGAT GGGTATGAAA TTGTCTTGTC TCAGAACCCA TCAACCGGAC GAATCATAAG   1200
CCAACAGTCT CGACAAATGA CTTCACTCGA CCATATGAGC AGTAATAGAA CCAATTCTCA   1260
AAGCAACAAA CTGCGCAATT CAAAGGAGCA GTGATCAGTC TTCCAGAAAG TCTACTTGAG   1320
TTTGTTCGTA TGTCAAAATC AAGTATCAAC CATAGAAATT TCCATTATAT TCGGAGTGTT   1380
TTAGTCAAGT TCTAGTAATA CCGCTGGAGT CATGATAGTT ATGACAGTAA TACCGCTGGA   1440
GTCAAGTTCT AGTAATACCG TTGGAGTCAA GTTATGATAG TTATTTAAAA ATTAGTATTT   1500
TATTACAAAT TTGTTATTGT TGTGAGACTT GTTTATTAAG TAAATGGAAA GTCTTATCAT   1560
TATTATCATT TGAGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA          1613
```

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 427 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: [lacuna]

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Phe Ser Arg Arg Ser Asn Ile Ser Asn Phe Ser Cys Cys Phe
1               5                   10                  15
Leu Val Ile Ile Val Leu Ser Leu His Cys Glu Asn His Ile Val Ser
                20                  25                  30
Ser Ser Ala Ser Arg Phe Ile Gln Thr Arg Gly Thr Arg Phe Val Leu
        35                  40                  45
```

Gly Gly Tyr Pro Phe Phe Phe Asn Gly Phe Asn Ser Tyr Trp Met Met
    50   55   60

His Val Ala Ala Glu Pro Ser Glu Arg His Lys Ile Ser Asn Val Phe
65   70   75   80

Arg Glu Ala Ala Ala Thr Gly Leu Thr Val Cys Arg Thr Trp Ala Phe
            85   90   95

Ser Asp Gly Gly Asp Arg Ala Leu Gln Met Ser Pro Gly Val Tyr Asp
           100   105   110

Glu Arg Val Phe Gln Ala Leu Asp Phe Val Val Ser Glu Ala Arg Lys
           115   120   125

Tyr Gly Val His Leu Ile Leu Ser Leu Thr Asn Asn Tyr Lys Asp Phe
           130   135   140

Gly Gly Arg Thr Gln Tyr Val Thr Trp Ala Lys Asn Ala Gly Val Gln
145   150   155   160

Val Asn Ser Asp Asp Asp Phe Tyr Thr Lys Asn Ala Val Lys Gly Tyr
           165   170   175

Tyr Lys Asn His Ile Lys Lys Val Leu Thr Arg Ile Asn Thr Ile Ser
           180   185   190

Arg Val Ala Tyr Lys Asp Asp Pro Thr Val Met Ala Trp Glu Leu Ile
           195   200   205

Asn Glu Pro Arg Cys Gln Val Asp Phe Ser Gly Lys Thr Leu Asn Ala
           210   215   220

Trp Val Gln Glu Met Ala Thr Tyr Val Lys Ser Leu Asp Asn Lys His
225   230   235   240

Leu Leu Glu Ile Gly Met Glu Gly Phe Tyr Gly Asp Ser Met Pro Gly
           245   250   255

Lys Lys Gln Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Thr
           260   265   270

Asn Asn Leu Ile Lys Glu Ile Asp Phe Ala Thr Ile His Ala Tyr Pro
           275   280   285

Asp Ile Trp Leu Ser Gly Gln Ser Asp Gly Ala Gln Met Met Phe Met
           290   295   300

Arg Arg Trp Met Thr Ser His Ser Thr Asp Ser Lys Thr Ile Leu Lys
           305   310   315   320

Lys Pro Leu Val Leu Ala Glu Phe Gly Lys Ser Ser Lys Asp Pro Gly
           325   330   335

```
Tyr Ser Leu Tyr Ala Arg Glu Ser Phe Met Ala Ala Ile Tyr Gly Asp
            340             345             350

Ile Tyr Arg Phe Ala Arg Arg Gly Gly Ile Ala Gly Gly Leu Val Trp
            355             360             365

Gln Ile Leu Ala Glu Gly Met Gln Pro Tyr Ala Asp Gly Tyr Glu Ile
        370             375             380

Val Leu Ser Gln Asn Pro Ser Thr Gly Arg Ile Ile Ser Gln Gln Ser
385             390             395             400

Arg Gln Met Thr Ser Leu Asp His Met Ser Ser Asn Arg Thr Asn Ser
            405             410             415

Gln Ser Asn Lys Leu Arg Asn Ser Lys Glu Gln
            420             425
```

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:


```
GGNATGGARG GNTTYTAYGG                                      20
```


(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:


```
TTTTTTTTTT TTTTT                                           15
```

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAATCTGTGC CCACTTG 17

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GTAAAACGAC GGCCAGT 17

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 base pairs

        (B) TYPE: nucleotide

        (C) STRANDEDNESS: single

        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: other nucleic acid

        (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGAAACAG CTATGAC 17

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: [lacuna]

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ser Phe Asn Phe Val Lys Thr Arg Gly Thr Glu Phe Val Met Asp Xaa
1   5   10   15

Arg Phe Leu Tyr Leu
            20

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 10 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: [lacuna]

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Thr Trp Ala Phe Ser Asp Gly Gly Tyr Arg
1   5   10

(2) INFORMATION FOR SEQ ID NO: 10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 amino acids

        (B) TYPE: amino acid

        (C) STRANDEDNESS: [lacuna]

        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Glu Tyr Asn Pro Gly Tyr Gln Val Gly Thr Asp Phe Ile Ser Asn Asn
1               5                   10                  15
```

```
Arg
```

(2) INFORMATION FOR SEQ ID NO: 11:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 36 base pairs

            (B) TYPE: nucleotide

            (C) STRANDEDNESS: single

            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid

            (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
GTCTTATCCC TGGATCCCGA AAATCATATA GTTTCT                    36
```

(2) INFORMATION FOR SEQ ID NO: 12:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 40 base pairs

            (B) TYPE: nucleotide

            (C) STRANDEDNESS: single

            (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: other nucleic acid

            (A) DESCRIPTION: /desc - "SYNTHETIC NUCLEOTIDE"

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```
GTACTCTGCA GACTTTCTGG AAGACTGATC ACTGCTCCTT               40
```